AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claim 1. (Currently Amended) A method for altering fiber development or properties of a fiber-producing plant comprising the step of providing cells of said plants a plant with a chimeric gene comprising the following operably linked DNA fragments:

a plant expressible promoter;

a the coding region from a-which when transcribed yields an RNA said RNA being capable of reducing the expression of an endogenous sucrose synthase gene, preferably an endogenous sucrose synthase gene expressed in fiber cells, preferably fiber initial cells; or capable of being translated into an active plant sucrose synthase gene protein; and

a transcription termination and polyadenylation signal which functions in said plant cells.

Claim 2. (Currently amended) The method according to claim 1, wherein said RNA is capable of being translated into an active plant sucrose synthase protein gene is at least 95% homologous to a DNA selected from the group consisting of the DNA of SEQ ID NO: 1 and DNA with GenBank accession number BM094593 (Glycine max); BM093753 (Glycine max); BM093753 (Glycine max); BM093158 (Glycine max); BM092695 (Glycine max); BM092443 (Glycine max); BM092322 (Glycine max); BM085310 (Glycine max); BM085020 (Glycine max); AY059416 (Zea mays); AF273253 (Beta vulgaris);

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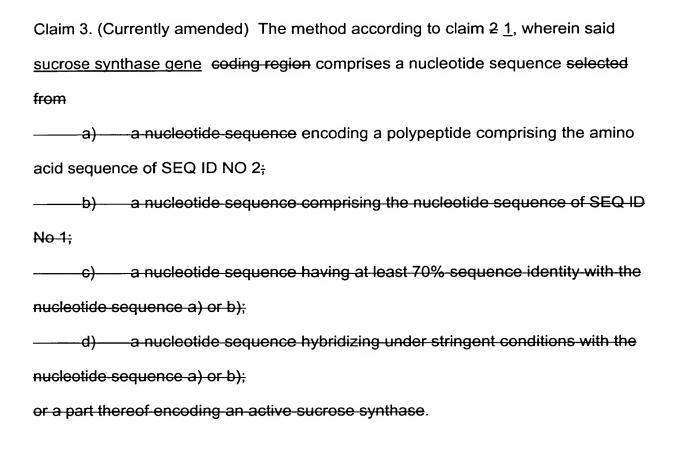
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(Lycopersicon esculentum); M18745 (Potato); L33244 (Zea mays); L22296 (Zea mays); and Z17959 (Arabidopsis thaliana).



Claim 4. (Withdrawn) The method according to claim 1, wherein said RNA is capable of reducing the expression of an endogenous sucrose synthase gene.

Claim 5. (Withdrawn) The method according to claim 4, wherein said coding region comprises a nucleotide sequence selected from the group consisting of

a nucleotide sequence comprising at least 19 or 25 contiguous nucleotides having at least 70% sequence identity to a nucleotide sequence encoding a

polypeptide comprising the amino acid sequence of SEQ ID NO 2 or the complement thereof; and

a nucleotide sequence comprising at least 25 contiguous nucleotides having at least 70% sequence identity to a nucleotide sequence encoding a polypeptide comprising the nucleotide sequence of SEQ ID No 1 or the complement thereof.

Claim 6. (Withdrawn) The method according to claim 5, wherein said coding region comprises the nucleotide sequence of SEQ ID No 1 from the nucleotide at position 2208 to the nucleotide at position 2598 or the complement thereof.

Claim 7. (Withdrawn) The method according to claim 5, wherein said coding region comprises both sense and antisense nucleotide sequences capable of forming a double stranded RNA molecule.

Claim 8. (Currently Amended) The method according to any one of claims 1, 2, or 3 1 to 7, wherein said promoter is a subterranean clover stunt virus promoter.

Claim 9. (Currently Amended) The method according to any one of claims 1, 2, or 3 1 to 7, wherein said fiber-producing plant is a cotton plant.

Claim 10. (Original) The method according to claim 8, wherein said fiber-producing plant is a cotton plant.

Claim 11. (Deleted)

Claim 12. (Currently amended) A method for improving fiber yield in a fiberproducing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments

a plant expressible promoter;

a the coding region from a DNA region capable of being translated into an active a sucrose synthase gene protein; and

a transcription termination and polyadenylation signal which functions in said plant cells.

Claim 13. (Currently amended) A method for improving fiber quality in a fiberproducing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments

a plant expressible promoter;

a the <u>coding region from</u> <u>DNA region capable of being translated into an active a sucrose synthase gene protein</u>; and

a transcription termination and polyadenylation signal which functions in said plant cells.

Claim 14. (Currently amended) A method for increasing seed size in a fiberproducing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments:

a seed-specific promoter;

a the <u>coding region from a DNA region capable of being translated into an active</u> sucrose synthase <u>gene protein</u>; and

a transcription termination and polyadenylation signal which functions in said plant cells.

Claim 15. (Currently Amended) A fiber-producing plant comprising in its genome a chimeric DNA comprising the following operably linked DNA fragments:

a plant expressible promoter;

a the coding region <u>from a which when transcribed yields an RNA said RNA</u>

synthase gene, preferably an endogenous sucrose synthase gene expressed in fiber cells, preferably fiber initial cells; or

capable of being translated into an active sucrose synthase gene protein; and

a transcription termination and polyadenylation signal which functions in said plant cells.

Claim 16. (Currently amended) A fiber-producing plant according to claim 15, wherein said RNA is capable of increasing the expression of an endogenous sucrose synthase gene, preferably an endogenous sucrose synthase gene expressed in fiber cells, preferably fiber initial cells and said fiber cells have an increased sucrose synthase activity compared to fiber cells of plant cells which do not comprise said chimeric DNA is at least 95% homologous to a DNA selected from the group

consisting of the DNA of SEQ ID NO: 1; DNA with GenBank accession number BM094593 (Glycine max); BM093753 (Glycine max); BM093158 (Glycine max); BM092695 (Glycine max); BM092443 (Glycine max); BM092322 (Glycine max); BM085310 (Glycine max); BM085020 (Glycine max); AY059416 (Zea mays); AF273253 (Beta vulgaris); L39940 (Oryza sativa); AJ316590 (Nostoc punctiforme); AJ316589 (Nostoc punctiforme); AJ316596 (Anabaena sp.); AJ316595(Anabaena sp.); AJ316584 (Anabaena sp.); BM005654 (Crocus sativus); BI973032 (Glycine max); BI971794 (Glycine max); AF367450 (Prunus persica); BI945506 (Glycine max); BI944973 (Glycine max); AF420224 (Carica papaya); BI788449 (Glycine max); BI788359 (Glycine max); BI787127 (Glycine max); BI787033(Glycine max); BI787000 (Glycine max); BI786823(Glycine max); BI784933 (Glycine max); BI784627 (Glycine max); BI700214 (Glycine max); BI699934 (Glycine max); BI699923 (Glycine max); BI699585(Glycine max); BI543240 (Sugar beet); BI498340 (Glycine max); BI471463 (Glycine max); BI427241(Glycine max); BI427174 (Glycine max); BI427022 (Glycine max); BI426915 (Glycine max); AF393809 (Apium graveolens); BI321173 (Glycine max); BI320832 (Glycine max); BI316894 (Glycine max); BI316826 (Glycine max); BI316405 (Glycine max); BI315949 (Glycine max); BI203222 (Lycopersicon esculentum); BI176503 (Solanum tuberosum); BG273882 (Grape berries); AY034958 (Arabidopsis thaliana); AF378187(Oryza sativa); BG790580 (Glycine max); BG790079 (Glycine max); BG726150 (Glycine max); BG654021 (Glycine max); BG653916 (Glycine max); BG653624 (Glycine max); BG652711(Glycine max); BG652507 (Glycine max); BG649914 (Glycine max); BG649831 (Glycine max); AJ309093 (Pinus pinaster); BG507656 (Glycine max); BG405632 (Glycine max); BG405474 (Glycine max); BG405204 (Glycine max);

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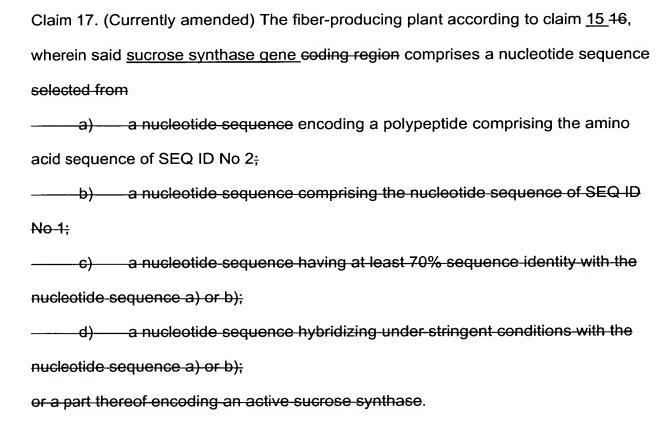
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(Solanum tuberosum); X73221 (H. vulgare); L32898 (Zea mays); F13913

(Arabidopsis thaliana); F13912 (Arabidopsis thaliana); U21129 (Solanum tuberosum); M26672 (Triticum aestivum); M26671 (Triticum aestivum); L19762

(Lycopersicon esculentum); M18745 (Potato); L33244 (Zea mays); L22296 (Zea mays); and Z17959 (Arabidopsis thaliana).



Claim 18. (Withdrawn) A fiber-producing plant according to claim 15, wherein said RNA is capable of reducing an endogenous sucrose synthase gene and said fiber cells have a reduced sucrose synthase activity compared to fiber cells of plant cells which do not comprise said chimeric DNA.

Claim 19. (Withdrawn) The fiber-producing plant according to claim 18, wherein said coding region comprises a nucleotide sequence selected from the group consisting of

a nucleotide sequence comprising at least 19 or 25 contiguous nucleotides having at least 70% sequence identity to a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID No 2 or the complement thereof; and

a nucleotide sequence comprising at least 19 or 25 contiguous nucleotides having at least 70% sequence identity to a nucleotide sequence encoding a polypeptide comprising the nucleotide sequence of SEQ ID No 1 or the complement thereof.

Claim 20. (Withdrawn) The fiber-producing plant according to claim 18, wherein said codign region comprises the nucleotide sequence of SEQ ID No 1 from the nucleotide at position 2208 to the nucleotide at position 2598 or the complement thereof.

Claim 21. (Currently Amended) The fiber-producing plant according to any one of claims 15, 16, or 17 15 to 20, wherein said plant is a cotton plant.

Claim 22. (Currently Amended) Seeds of a plant according to any one of claims 15, 16, or 17 15 to 20.

Claim 23. (Original) Seeds of a plant according to claim 21.

Claim 24. (Currently Amended) Fibers with altered development or properties, isolated from plants according to any one of claims 15, 16, or 17 15 to 20.

Claim 25. (Original) Fibers with altered development or properties, isolated from plants according to claim 21.

Claim 26. (Currently Amended) Plants obtained through the methods of any one of claims 1, 2, or 3 1 to 7.

Claim 27. (Original) Plants obtained through the methods of claim 8.

Claim 28. (Original) Plants obtained through the methods of claim 9.

Claim 29. (Original) Plants obtained through the methods claim 10.

Claim 30. (Currently Amended) Plants obtained through the methods of any one of claims 41 12, 13, or to 14.